

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2003, 09:20:45 : Search time 48 Seconds  
(without alignments)  
5513.793 Million cell updates/sec

Title: US-10-021-811-35  
Perfect score: 863  
Sequence: 1 gcacgagctctatcacacac.....aaaaaaaaaaaaaaaaaaaa 863

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size : 60

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
---------------	-------	----------------	--------	----	-------------

No matches found

Search completed: February 18, 2003, 10:32:30  
Job time : 48 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2003, 09:21:50 ; Search time 59 Seconds  
(without alignments)  
7449.937 Million cell updates/sec

Title: US-10-021-811-35  
Perfect score: 863  
Sequence: 1 gcacgagctctatcacac.....aaaaaaaaaaaaaaaaa 863

Scoring table:  
OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 424239 seqs, 254661826 residues

Word size : 60

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PublishedApplications\_NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:  
13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	863	100.0	863	9	US-10-021-811-35
					Sequence 35, Appl

ALIGNMENTS

RESULT 1  
US-10-021-811-35  
; Sequence 35, Application US/10021811  
; Publication No. US20030024007A1  
; GENERAL INFORMATION:  
; APPLICANT: Cahoon, Rebecca E.  
; APPLICANT: Fang, Yiwen  
; APPLICANT: Odell, Joan  
; APPLICANT: Wang, Zude  
; TITLE OF INVENTION: Plant Myb Transcription Factor Homologs  
; FILE REFERENCE: B01294 US NA  
; CURRENT APPLICATION NUMBER: US/10/021.811  
; CURRENT FILING DATE: 2001-12-14

; PRIOR APPLICATION NUMBER: 60/110,609  
; PRIOR FILING DATE: 1998-December-02  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 35  
; LENGTH: 863  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-10-021-811-35

Query Match 100.0%; Score 863; DB 9; Length 863;  
Best Local Similarity 100.0%; Pred. No. 4.6e-301;  
Matches 863; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAGGAGCTCTATCACACACACAAAGTCAATGGATATAAAAAACAACAGTGTAAAGCTCTCA 60  
DB 1 GCAGGAGCTCTATCACACACACAAAGTCAATGGATATAAAAAACAACAGTGTAAAGCTCTCA 60  
QY 61 AGATCCTGAAGTGAGAAAAAGGGCTTGGACAATGGAAGAAGACTTGGATCTTGATGAACTA 120  
DB 61 AGATCCTGAAGTGAGAAAAAGGGCTTGGACAATGGAAGAAGACTTGGATCTTGATGAACTA 120  
QY 121 TATTGCAAAATCATGGGGAAGGTGTTTGGAACTCTTTGGCCAAAGCTGCTGGTCTCAACG 180  
DB 121 TATTGCAAAATCATGGGGAAGGTGTTTGGAACTCTTTGGCCAAAGCTGCTGGTCTCAACG 180  
QY 181 TAACGAAAGAGTTGCCGGCTAAGGTGGCTAAATTTACCTCCGCTCCTGATGTTAGAAAGG 240  
DB 181 TAACGAAAGAGTTGCCGGCTAAGGTGGCTAAGGTGGCTAATTTACCTCCGCTCCTGATGTTAGAAAGG 240  
QY 241 GAATATTACACCCGAGGAACAACCTTTTGTATTTGAGTCTCCAGCAAGTGGGGAACAG 300  
DB 241 GAATATTACACCCGAGGAACAACCTTTTGTATTTGAGTCTCCAGCAAGTGGGGAACAG 300  
QY 301 GTGTCCTCAAAATGCCCAAGCATCTACCTGGAAGACTGATAAAGTCAAGAACTATTG 360  
DB 301 GTGTCCTCAAAATGCCCAAGCATCTACCTGGAAGACTGATAAAGTCAAGAACTATTG 360  
QY 361 GAGGACAAGGATCCAGAAAGCAGACATCAAGCAAGCTGAGAAGCTTTTCAGCAACAGAGTAGTAA 420  
DB 361 GAGGACAAGGATCCAGAAAGCAGACATCAAGCAAGCTGAGAAGCTTTTCAGCAACAGAGTAGTAA 420  
QY 421 TAATTCAGATAAATGATCAGCAAGCTAGCACTAGCCATGTTTCCACCAGTGGCTGAGCC 480  
DB 421 TAATTCAGATAAATGATCAGCAAGCTAGCACTAGCCATGTTTCCACCAGTGGCTGAGCC 480  
QY 481 CATGGAGATGTTTCTCCACCTGTTATCAAGGAATGTTAGAGCCATTTTCAACTCAGTT 540  
DB 481 CATGGAGATGTTTCTCCACCTGTTATCAAGGAATGTTAGAGCCATTTTCAACTCAGTT 540  
QY 541 CCCTACAATTAATCCTGATCAATCCAGTGTGTTGTACCAATGACAACAAACATTAAC 600  
DB 541 CCCTACAATTAATCCTGATCAATCCAGTGTGTTGTACCAATGACAACAAACATTAAC 600  
QY 601 TTGAGCATGGAGATAGCTGGTCAATGCAATTTACTGAACGGTGATTAATATATTCAAG 660  
DB 601 TTGAGCATGGAGATAGCTGGTCAATGCAATTTACTGAACGGTGATTAATATATTCAAG 660  
QY 661 ATAAACCTTAAGTGTGCAAGTTCATGAAGCTGGAATGCTTGTGGATTAACACATATTAT 720  
DB 661 ATAAACCTTAAGTGTGCAAGTTCATGAAGCTGGAATGCTTGTGGATTAACACATATTAT 720  
QY 721 TGGGTTTGTATATAGTAGTGGATGTTTGGTGTGCGTAGCATTATTAGTATGTGC 780  
DB 721 TGGGTTTGTATATAGTAGTGGATGTTTGGTGTGCGTAGCATTATTAGTATGTGC 780  
QY 781 TGTAAATATACGAGATYTTATTAACATATATCGCATGCTTTATATAAAAAA 840  
DB 781 TGTAAATATACGAGATYTTATTAACATATATCGCATGCTTTATATAAAAAA 840  
QY 841 AAAAAAAAAAAAAAAAAAAAAA 863  
DB 841 AAAAAAAAAAAAAAAAAAAAAA 863

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2003, 08:51:00 ; Search time 2196 Seconds  
(without alignments)  
11437.032 Million cell updates/sec

Title: US-10-021-811-35

Perfect score: 863

Sequence: 1 gcacgagctctatcacacac.....aaaaaaaaaaaaaaaaaaaa 863

Scoring table:

OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 60

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: go\_un.\*
- 14: gb\_vl.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vl.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rod.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
------------	-------	-------	--------	----	----	-------------

No matches found

Search completed: February 18, 2003, 10:02:37  
Job time : 2196 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2003, 08:14:20 ; Search time 220 Seconds  
(without alignments)  
8833.975 Million cell updates/sec

Title: US-10-021-811-35  
Perfect score: 863  
Sequence: 1 gcagagctctatcacac.....aaaaaaaaaaaaaaaa 863

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 60

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_101002:\*  
1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*  
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*  
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*  
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*  
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*  
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*  
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*  
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*  
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*  
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*  
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*  
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*  
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*  
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*  
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*  
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*  
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:\*  
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*  
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*  
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*  
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
-----				

No matches found

Search completed: February 18, 2003, 09:25:40  
Job time : 221 secs

